

HEAVY CONSTANT CHAINS CH3 REGION

	EU INDEX	OU INDEX	INVARIANT RESIDUES	1 HUMAN IGH CL	2 HUMAN IGH CL	3 GAL OU	4 OU	5 BOT	6 X17115 CL	7 GLI	8 HUMAN IGH MEMB CL	9 WAH -65 CL	10 NIG -65 CL	11 ERI	12 HUMAN IGH CL	13 HUMAN IGH MEMB CL	14 HUMAN IGH CL	15 OMH CL	16 HER CL	17 FRO CL	18 CON CL	19 WIS CL
361	341	340		ASP	ASP	ASP	ASP	ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLY	GLY			GLY	
362	342	341		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN			GLN	
363	343	342		ASP	ASP	ASP	ASP	ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLN	GLN			GLN	
364	344	343		THR	THR	THR	THR	THR	THR	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ARG	ARG			ARG	
365	345	344		ALA	ALA	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL	
366	346	345		ILE	ILE	ILE	ILE	ILE	ILE	LYS	LYS	LYS	LYS	LYS	LYS	LYS	PRO	PRO			PRO	
367	347	346		ALA	ALA	ALA	ALA	ALA	ALA	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	
367A			PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
367B				---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
368	347	346		ARG	ARG	ARG	ARG	ARG	ARG	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLN			GLN	
369	348	347		VAL	VAL	VAL	VAL	VAL	VAL	SER	SER	SER	SER	SER	SER	SER	VAL	VAL			VAL	
370	349	348		PHE	PHE	PHE	PHE	PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	TYR	TYR			TYR	
371	350	349		ALA	ALA	ALA	ALA	ALA	ALA	ASN	ASN	ASN	ASN	ASN	ASN	ASN	THR	THR			THR	
372	351	350		ILE	ILE	ILE	ILE	ILE	ILE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	
373	352	351		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO			PRO	
374	353	352		PRO	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO			PRO	
375	354	353		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER			SER	
376	355	354		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
377	356	355		PHE	PHE	PHE	PHE	PHE	PHE	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP			ASP	
378	357	356		ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO			PRO	
379	358	357		SER	SER	SER	SER	SER	SER	---	---	---	---	---	---	---	---	---			---	
380	359	358		ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	---	---			---	
381	360	359		PHE	PHE	PHE	PHE	PHE	PHE	---	---	---	---	---	---	---	---	---			---	
382	361	360		LEU	LEU	LEU	LEU	LEU	LEU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU			GLU	
383	362	361		THR	THR	THR	THR	THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA			ALA	
384	363	362		LYS	LYS	LYS	LYS	LYS	LYS	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASN	ASN			ASN	
385	364	363		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	GLN	GLN			GLN	
386	365	364		THR	THR	THR	THR	THR	THR	TRP	TRP	TRP	TRP	TRP	TRP	TRP	VAL	VAL			VAL	
387	366	365		LYS	LYS	LYS	LYS	LYS	LYS	LEU	LEU	LEU	LEU	LEU	LEU	LEU	SER	SER			SER	
388	367	366		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	
389	368	367		THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	LEU	THR	THR			THR	
390	369	368		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS	
391	370	369		LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL	
392	371	370		VAL	VAL	VAL	VAL	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	LYS	LYS			LYS	
393	372	371		THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	SER	GLY	GLY			GLY	
394	373	372		ASP	ASP	ASP	ASP	ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	PHE	PHE			PHE	
395	374	373		LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PHE	TYR	TYR			TYR	
396	375	374		THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	SER	PRO	PRO			PRO	
397	376	375		TYR	TYR	TYR	TYR	TYR	TYR	PRO	PRO	PRO	PRO	PRO	PRO	PRO	SER	SER			SER	
398	377	376		ASP	ASP	ASP	ASP	ASP	ASP	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASP	ASP			ASP	
399	378	377		---	---	---	---	---	---	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ALA	ALA			ALA	
400	379	378		SER	SER	SER	SER	SER	SER	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL			VAL	
401	380	379		VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	---	---	---	---	---	---			---	
402	381	380		THR	THR	THR	THR	THR	THR	ILE	ILE	ILE	ILE	ILE	ILE	ILE	THR	THR			THR	
403	382	381		ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	---	---			---	
404	383	382		SER	SER	SER	SER	SER	SER	MET	MET	MET	MET	MET	MET	MET	GLU	GLU			GLU	
405	384	383		TRP	TRP	TRP	TRP	TRP	TRP	LEU	LEU	LEU	LEU	LEU	LEU	LEU	TRP	TRP			TRP	
406	385	384		THR	THR	THR	THR	THR	THR	GLU	GLU	GLU	GLU	GLU	GLU	GLU	SER	SER			SER	
407	386	385		ARG	ARG	ARG	ARG	ARG	ARG	---	---	---	---	---	---	---	---	---			---	
408	387	386		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
409	388	387		---	---	---	---	---	---	ASP	ASP	ASP	ASP	ASP	ASP	ASP	---	---			---	
410	389	388		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	SER			SER	
411	390	389		ASN	ASN	ASN	ASN	ASN	ASN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLY	GLY			GLY	
412	391	390		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
413	392	391		GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---	---			---	
414	393	392		GLU	GLU	GLU	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLN	GLN			GLN	
415	394	393		ALA	ALA	ALA	ALA	ALA	ALA	THR	THR	THR	THR	THR	THR	THR	PRO	PRO			PRO	
416	395	394		VAL	VAL	VAL	VAL	VAL	VAL	SER	SER	SER	SER	SER	SER	SER	GLU	GLU			GLU	
417	396	395		---	---	---	---	---	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASN	ASN			ASN	
418	397	396		LYS	LYS	LYS	LYS	LYS	LYS	PHE	PHE	PHE	PHE	PHE	PHE	PHE	TYR	TYR			TYR	
419	398	397		THR	THR	THR	THR	THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LYS	LYS			LYS	
420	399	398		HIS	HIS	HIS	HIS	HIS	HIS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	THR	THR			THR	
421	400	399		ASN	ASN	ASN	ASN	ASN	ASN	ARG	ARG	ARG	ARG	ARG	ARG	ARG	THR	THR			THR	
422	401	400		ILE	ILE	ILE	ILE	ILE	ILE	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO			PRO	
423	402	401		SER	SER	SER	SER	SER	SER	PRO	PRO	PRO	PRO	PRO	PRO	PRO	MET	MET			MET	
424	403	402		GLU	GLU	GLU	GLU	GLU	GLU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU	LEU			LEU	
425	404	403		SER	SER	SER	SER	SER	SER	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ASP	ASP			ASP	
426	405	404		SER	SER	SER	SER	SER	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER	SER			SER	
427	406	405		HIS	HIS	HIS	HIS	HIS	HIS	---	---	---	---	---	---	---	---	---			---	
428	407	406		PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---	---	---	---	---			---	
429	408	407		ASN	ASN	ASN	ASN	ASN	ASN	SER	SER	SER	SER	SER	SER	SER	ASP	ASP			ASP	
430	409	408		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
431	410	409		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
432	411	410		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			---	
433	412	411		ALA	ALA	ALA	ALA	ALA	ALA	THR	THR	THR	THR	THR	THR	THR	GLY	GLY			GLY	
434	413	412		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER	SER			SER	
435	414	413		PHE	PHE	PHE	PHE	PHE	PHE	THR	THR	THR	THR	THR	THR	THR	PHE	PHE			PHE	
436	415	414		SER	SER	SER	SER	SER	SER	TRP	TRP	TRP	TRP	TRP	TRP	TRP	LEU	LEU			LEU	
437	416	415		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA			ALA	
438	417	416		VAL	VAL	VAL	VAL	VAL	VAL	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TYR	TYR			TYR	
439	418	417		GLY	GLY	GLY	GLY	GLY	GLY	SER	SER	SER	SER	SER	SER	SER	SER	SER			SER	
440	419	418		GLU	GLU	GLU	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LYS	LYS			LYS	
441	420	419		ALA	ALA	ALA	ALA	ALA	ALA	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	
442	421	420		SER	SER	SER	SER	SER	SER	ARG	ARG	ARG	ARG	ARG	ARG	ARG	THR	THR			THR	
443	422	421		ILE	ILE	ILE	ILE	ILE	ILE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL	
444	423	422		CYS	CYS	CYS	CYS	CYS	CYS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ASP	ASP			ASP	
445	424	423		GLU	GLU	GLU	GLU	GLU	GLU	ALA	ALA	ALA										

HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU	OU	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
INDEX	INDEX	SPA	ZUC	ZUC	KUP	BRU	JIR	CHA	GOE	EU	NIE	CRA	VAU	LEB	EST	YOK	SAC	HUMAN	KOL	MCG	LEC	DOB	BUR	TRO	CAR
361	341		GLY				GLY		GLY	GLY	GLY							GLY	GLY				GLY	GLY	
362																									
363	342	341	GLN				GLN		GLN	GLN	GLN							GLN	GLN				ASN	ASN	
364	343	342	PRO				PRO		PRO	PRO	PRO							PRO	PRO				THR	THR	
365	344	343	ARG				ARG		ARG	ARG	ARG							ARG	ARG				PHE	PHE	
366	345	344	GLX				GLU		GLU	GLU	GLU							GLU	GLU				ARG	ARG	
367	346	345	PRO				PRO		PRO	PRO	PRO							PRO	PRO				PRO	PRO	
367A																									
367B																									
368	347	346	GLX				GLN		GLN	GLN	GLN							GLN	GLN				GLN	GLN	
369	348	347	VAL				VAL		VAL	VAL	VAL							VAL	VAL				VAL	VAL	
370	349	348	TYR				TYR		TYR	TYR	TYR							TYR	TYR				HIS	HIS	
371	350	349	THR				THR		THR	THR	THR							THR	THR				LEU	LEU	
372	351	350	LEU				LEU		LEU	LEU	LEU							LEU	LEU				LEU	LEU	
373	352	351	PRO				PRO		PRO	PRO	PRO							PRO	PRO				PRO	PRO	
374	353	352	PRO				PRO		PRO	PRO	PRO							PRO	PRO				PRO	PRO	
375	354	353	SER				SER		SER	SER	SER							SER	SER				PRO	PRO	
376	355	354	ARG				ARG		ARG	ARG	ARG							ARG	ARG				SER	SER	
377	356	355	GLU				GLU		GLU	GLU	ASP							ASP	GLU				GLX	GLX	
378	357	356	GLU				GLU		GLU	GLU	GLU							GLU	GLU				GLX	GLN	
379																									
380	358	357																							
381	358	358	MET				MET		MET	MET	LEU							LEU	MET				ALA	ALA	
382	359	359	THR				THR		THR	THR	THR							THR	THR				LEU	LEU	
383	360	360	LYS				LYS		LYS	LYS	LYS							LYS	LYS				ASN	ASN	
384	361	361					ASN		ASN	ASN	ASN							ASN	ASN				GLX	GLN	
385	362	362	GLN				GLN		GLN	GLN	GLN							GLN	GLN				LEU	LEU	
386	363	363	VAL				VAL		VAL	VAL	VAL							VAL	VAL				VAL	VAL	
387	364	364	SER				SER		SER	SER	SER							SER	SER				THR	THR	
388	365	365	LEU				LEU		LEU	LEU	LEU							LEU	LEU				LEU	LEU	
389	366	366	THR				THR		THR	THR	THR							THR	THR				THR	THR	
390	367	367	CYS				CYS		CYS	CYS	CYS							CYS	CYS				CYS	CYS	
391	368	368	LEU				LEU		LEU	LEU	LEU							LEU	LEU				LEU	LEU	
392	369	369	VAL				VAL		VAL	VAL	VAL							VAL	VAL				ALA	ALA	
393	370	370	LYS				LYS		LYS	LYS	LYS							LYS	LYS				ARG	ARG	
394	371	371	GLY				GLY		GLY	GLY	GLY							GLY	GLY				GLY	GLY	
395	372	372	PHE				PHE		PHE	PHE	PHE							PHE	PHE				PHE	PHE	
396	373	373	TYR				TYR		TYR	TYR	TYR							TYR	TYR				TYR	TYR	
397	374	374	PRO				PRO		PRO	PRO	PRO							PRO	PRO				PRO	PRO	
398	375	375	SER				SER		SER	SER	SER							SER	SER				LYS	LYS	
399	376	376	ASP				ASP		ASP	ASP	ASP							ASP	ASP				ASP	ASP	
400	377	377	ILE				ILE		ILE	ILE	ILE							ILE	ILE				VAL	VAL	
401	378	378	ALA				ALA		ALA	ALA	ALA							ALA	ALA				LEU	LEU	
402	379	379	MET				MET		MET	MET	MET							VAL	VAL				VAL	VAL	
403																									
404																									
405	380	381	GLU				GLU		GLU	GLU	GLU							GLU	GLU				ARG	ARG	
406	381	382	TRP				TRP		TRP	TRP	TRP							TRP	TRP				TRP	TRP	
407	382	383	GLU				GLU		GLU	GLU	GLU							GLU	GLU				LEU	LEU	
408	383	384	SER				SER		SER	SER	SER							SER	SER				SER	SER	
409																									
410	384	385	SER				ASP		ASN	ASN	ASN							ASN	ASN				GLN	GLN	
411	385	386	GLY				GLY		ASP	ASP	ASP							GLY	ASP				GLY	GLY	
412																							GLN	GLN	
413																									
414	386	387	GLN				GLU		GLY	GLY	GLY							GLY	GLY				GLU	GLU	
415	387	388	PRO				PRO		GLU	GLU	GLU							GLN	GLN				LEU	LEU	
416	388	389	GLU				GLU		PRO	PRO	PRO							PRO	PRO				PRO	PRO	
417	389	390	ASN				ASN		GLU	GLU	GLU							GLU	GLU				ARG	ARG	
418	390	391	ASN				ASN		ASN	ASN	ASN							ASN	ASN				GLU	GLU	
419	391	392	TYR				TYR		TYR	TYR	TYR							ASN	ASN				LYS	LYS	
420	392	393	ASN				LYS		LYS	LYS	LYS							LYS	LYS				TYR	TYR	
421	393	394	THR				THR		LYS	LYS	LYS							THR	THR				LEU	LEU	
422	394	395	THR				THR		THR	THR	THR							THR	THR				TRP	TRP	
423	395	396	PRO				PRO		THR	THR	THR							THR	THR				ALA	ALA	
424	396	397	PRO				PRO		PRO	PRO	PRO							PRO	PRO				SER	SER	
425	397	398	MET				VAL		VAL	VAL	VAL							VAL	VAL				ARG	ARG	
426	398	399	LEU				LEU		VAL	VAL	VAL							VAL	VAL				GLN	GLN	
427	399	400	ASP				ASP		LEU	LEU	LEU							ASP	ASP				GLU	GLN	
428	400	401	SER				SER		ASP	ASP	ASP							SER	SER				PRO	PRO	
429									ASP	ASP	ASP							SER	SER				SER	SER	
430	401	402	ASP				ASP		ASP	ASP	ASP							ASP	ASP				GLN	GLN	
431																							GLY	GLY	
432																							THR	THR	
433	402	403	GLY				GLY		GLY	GLY	GLY							GLY	GLY				THR	THR	
434	403	404	SER				SER		SER	SER	SER							SER	SER				THR	THR	
435	404	405	PHE				PHE		PHE	PHE	PHE							PHE	PHE				PHE	PHE	
436	405	406	PHE				PHE		PHE	PHE	PHE							PHE	PHE				ALA	ALA	
437	406	407	LEU				LEU		PHE	PHE	PHE							LEU	LEU				VAL	VAL	
438	407	408	TYR				TYR		LEU	LEU	LEU							TYR	TYR				THR	THR	
439	408	409	SER				SER		TYR	TYR	TYR							TYR	TYR				THR	THR	
440	409	410	LYS				LYS		SER	SER	SER							SER	SER				THR	THR	
441	410	411	LEU				LEU		LYS	LYS	LYS							LYS	LYS				ILE	ILE	
442	411	412	THR				THR		LEU	LEU	LEU							THR	THR				LEU	LEU	
443	412	413	VAL				VAL		THR	THR	THR							THR	THR				ARG	ARG	
444	413	414	ASP				ASP		VAL	VAL															

BEST AVAILABLE COPY

HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	63 HUMAN IGA2 'CL	64 HUMAN IGA2 'CL	65 HUMAN IGA2 'CL	66 IGM 'CL	67 IGM 'CL	68 IGM-b 'CL	69 MUTANT 'CL	70 MOPC 104E	71 MOPC 104E MEMB 'CL	72 HPC76 'CL	73 G8 CA 'CL	74 GAT50 'CL	75 IGD 'CL	76 IGD SECR 'CL	77 IGD MEMB 'CL	78 B1-8 DELTA	79 MOUSE 1003 'CL	80 1003 MEMB 'CL	81 1003 'CL
361	341		GLY	GLY	---	---	---	---	---	---	---	---	---	GLY	---	---	---	GLY	---	---
362	342	340	---	---	SER	SER	SER	---	SER	---	---	---	---	ALA	---	---	---	---	---	---
363	342	342	ASN	ASN	PRO	PRO	PRO	---	PRO	---	---	---	---	ALA	---	---	---	---	---	---
364	343	343	THR	THR	THR	THR	THR	---	THR	---	---	---	---	ALA	---	---	---	---	---	---
365	344	343	PHE	PHE	THR	THR	THR	---	THR	---	---	---	---	PRO	---	---	---	---	---	---
366	345	344	ARG	ARG	ASP	ASP	ASP	---	ASP	---	---	---	---	SER	---	---	---	---	---	---
367A	346	345	PRO	PRO	ILE	ILE	ILE	---	ILE	---	---	---	---	ASN	---	---	---	---	---	---
367B	347	346	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
368	347	346	GLU	GLU	LEU	LEU	LEU	---	LEU	---	---	---	---	LEU	---	---	---	---	---	---
369	348	347	VAL	VAL	THR	THR	THR	---	ASN	---	---	---	---	THR	---	---	---	---	---	---
370	348	348	HIS	HIS	PHE	PHE	PHE	---	PHE	---	---	---	---	VAL	---	---	---	---	---	---
371	350	349	LEU	LEU	THR	THR	THR	---	THR	---	---	---	---	ASN	---	---	---	---	---	---
372	351	350	LEU	LEU	ILE	ILE	ILE	---	ILE	---	---	---	---	THR	---	---	---	---	---	---
373	352	351	PRO	PRO	PRO	PRO	PRO	---	PRO	---	---	---	---	LEU	---	---	---	---	---	---
374	353	352	PRO	PRO	PRO	PRO	PRO	---	PRO	---	---	---	---	THR	---	---	---	---	---	---
375	354	353	PRO	PRO	SER	SER	SER	---	SER	---	---	---	---	THR	---	---	---	---	---	---
376	355	354	SER	SER	---	---	---	---	---	---	---	---	---	SER	---	---	---	---	---	---
377	356	355	GLU	GLU	PHE	PHE	PHE	---	PHE	---	---	---	---	THR	---	---	---	---	---	---
378	357	355	GLU	GLU	ALA	ALA	ALA	---	ALA	---	---	---	---	HIS	---	---	---	---	---	---
379	358	356	---	---	ASP	ASP	ASP	---	ASP	---	---	---	---	---	---	---	---	---	---	---
380	358	357	LEU	LEU	ILE	ILE	ILE	---	ILE	---	---	---	---	---	---	---	---	---	---	---
381	358	358	ALA	ALA	PHE	PHE	PHE	---	PHE	---	---	---	---	PRO	---	---	---	---	---	---
382	359	359	LEU	LEU	LEU	LEU	LEU	---	LEU	---	---	---	---	GLU	---	---	---	---	---	---
383	360	360	ASN	ASN	SER	SER	SER	---	SER	---	---	---	---	MET	---	---	---	---	---	---
384	361	361	GLU	GLU	LYS	LYS	LYS	---	LYS	---	---	---	---	SER	---	---	---	---	---	---
385	362	362	LEU	LEU	SER	SER	SER	---	SER	---	---	---	---	SER	---	---	---	---	---	---
386	363	363	VAL	VAL	ALA	ALA	ALA	---	ALA	---	---	---	---	THR	---	---	---	---	---	---
387	364	364	THR	THR	ASN	ASN	ASN	---	ASN	---	---	---	---	LEU	---	---	---	---	---	---
388	365	365	LEU	LEU	LEU	LEU	LEU	---	LEU	---	---	---	---	LEU	---	---	---	---	---	---
389	366	366	THR	THR	THR	THR	THR	---	THR	---	---	---	---	LEU	---	---	---	---	---	---
390	367	367	CYS	CYS	CYS	CYS	CYS	---	CYS	---	---	---	---	CYS	---	---	---	---	---	---
391	368	368	LEU	LEU	LEU	LEU	LEU	---	LEU	---	---	---	---	GLU	---	---	---	---	---	---
392	369	369	ALA	ALA	VAL	VAL	VAL	---	VAL	---	---	---	---	VAL	---	---	---	---	---	---
393	370	370	ARG	ARG	SER	SER	SER	---	SER	---	---	---	---	SER	---	---	---	---	---	---
394	371	371	GLY	GLY	ASN	ASN	ASN	---	ASN	---	---	---	---	GLY	---	---	---	---	---	---
395	372	372	PHE	PHE	LEU	LEU	LEU	---	LEU	---	---	---	---	PHE	---	---	---	---	---	---
396	373	373	SER	SER	ALA	ALA	ALA	---	ALA	---	---	---	---	PHE	---	---	---	---	---	---
397	374	374	PRO	PRO	THR	THR	THR	---	THR	---	---	---	---	PRO	---	---	---	---	---	---
398	375	375	LYS	LYS	TYR	TYR	TYR	---	TYR	---	---	---	---	GLU	---	---	---	---	---	---
399	376	376	ASP	ASP	GLU	GLU	GLU	---	GLU	---	---	---	---	ASN	---	---	---	---	---	---
400	377	377	VAL	VAL	---	---	---	---	---	---	---	---	---	ILE	---	---	---	---	---	---
401	378	378	LEU	LEU	THR	THR	THR	---	THR	---	---	---	---	HIS	---	---	---	---	---	---
402	379	379	VAL	VAL	LEU	LEU	LEU	---	LEU	---	---	---	---	LEU	---	---	---	---	---	---
403	379	379	---	---	ASN	SER	ASN	---	THR	---	---	---	---	---	---	---	---	---	---	---
404	380	380	---	---	ILE	ILE	ILE	---	ILE	---	---	---	---	---	---	---	---	---	---	---
405	380	381	ARG	ARG	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	---	---	---
406	381	382	TRP	TRP	TRP	TRP	TRP	---	TRP	---	---	---	---	TRP	---	---	---	---	---	---
407	382	383	LEU	LEU	ALA	ALA	ALA	---	ALA	---	---	---	---	GLU	---	---	---	---	---	---
408	383	384	---	---	SER	SER	SER	---	SER	---	---	---	---	GLY	---	---	---	---	---	---
409	384	385	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
410	385	386	GLN	GLN	GLN	GLN	GLN	---	GLN	---	---	---	---	VAL	---	---	---	---	---	---
411	385	386	SER	SER	SER	SER	SER	---	SER	---	---	---	---	HIS	---	---	---	---	---	---
412	386	387	GLN	GLN	---	---	---	---	---	---	---	---	---	SER	---	---	---	---	---	---
413	387	388	---	---	---	---	---	---	---	---	---	---	---	LYS	---	---	---	---	---	---
414	388	389	GLU	GLU	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
415	389	390	LEU	LEU	GLY	GLY	GLY	---	GLY	---	---	---	---	LYS	---	---	---	---	---	---
416	390	391	PRO	PRO	GLU	GLU	GLU	---	GLU	---	---	---	---	SER	---	---	---	---	---	---
417	391	392	ARG	ARG	PRO	PRO	PRO	---	PRO	---	---	---	---	THR	---	---	---	---	---	---
418	392	393	GLU	GLU	LEU	LEU	LEU	---	LEU	---	---	---	---	ASN	---	---	---	---	---	---
419	393	394	LYS	LYS	GLU	GLU	GLU	---	GLU	---	---	---	---	---	---	---	---	---	---	---
420	394	395	TYR	TYR	THR	THR	THR	---	THR	---	---	---	---	PHE	---	---	---	---	---	---
421	395	396	LEU	LEU	LYS	LYS	LYS	---	LYS	---	---	---	---	THR	---	---	---	---	---	---
422	396	397	THR	THR	ILE	ILE	ILE	---	ILE	---	---	---	---	ALA	---	---	---	---	---	---
423	397	398	TRP	TRP	LYS	LYS	LYS	---	LYS	---	---	---	---	ASN	---	---	---	---	---	---
424	398	399	---	---	ALA	ALA	ALA	---	ALA	---	---	---	---	---	---	---	---	---	---	---
425	399	400	SER	SER	ILE	ILE	ILE	---	ILE	---	---	---	---	PRO	---	---	---	---	---	---
426	400	401	ARG	ARG	MET	MET	MET	---	MET	---	---	---	---	THR	---	---	---	---	---	---
427	401	402	GLN	GLN	SER	SER	SER	---	SER	---	---	---	---	ALA	---	---	---	---	---	---
428	402	403	GLU	GLU	HIS	HIS	HIS	---	HIS	---	---	---	---	GLN	---	---	---	---	---	---
429	403	404	PRO	PRO	PRO	PRO	PRO	---	PRO	---	---	---	---	PRO	---	---	---	---	---	---
430	404	405	SER	SER	---	---	---	---	---	---	---	---	---	GLY	---	---	---	---	---	---
431	405	406	GLN	GLN	ASN	ASN	ASN	---	ASN	---	---	---	---	---	---	---	---	---	---	---
432	406	407	GLY	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
433	407	408	THR	THR	THR	THR	THR	---	THR	---	---	---	---	---	---	---	---	---	---	---
434	408	409	THR	THR	GLY	GLY	GLY	---	GLY	---	---	---	---	GLY	---	---	---	---	---	---
435	409	410	PHE	TYR	PHE	PHE	PHE	---	PHE	---	---	---	---	THR	---	---	---	---	---	---
436	410	411	ALA	SER	SER	SER	SER	---	SER	---	---	---	---	PHE	---	---	---	---	---	---
437	411	412	VAL	VAL	ALA	ALA	ALA	---	ALA	---	---	---	---	THR	---	---	---	---	---	---
438	412	413	THR	THR	LYS	LYS	LYS	---	LYS	---	---	---	---	---	---	---	---	---	---	---
439	413	414	SER	SER	GLY	GLY	GLY	---	GLY	---	---	---	---	SER	---	---	---	---	---	---
440	414	415	ILE	ILE	VAL	VAL	VAL	---	VAL	---	---	---	---	VAL	---	---	---	---	---	---
441	415	416	LEU	LEU	ALA	ALA	ALA	---	ALA	---	---	---	---	ALA	---	---	---	---	---	---
442	416	417	ARG	ARG	SER	SER	SER	---	SER	---	---	---	---	ARG	---	---	---	---	---	---
443	417	418	VAL	VAL	VAL	VAL	VAL	---	VAL	---	---	---	---	LEU	---	---	---	---	---	---
444	418	419	ALA	ALA	CYS	CYS	CYS	---	CYS	---	---	---	---	PRO	---	---	---	---	---	---
445	419	420	ALA	ALA	VAL	VAL	VAL	---	VAL	---	---	---	---	VAL	---	---	---	---	---	---
446	420	421	GLU	GLU	GLU	GLU	GLU	---	GLU	---	---	---	---	THR	---	---	---	---	---	---
447	421	422	ASP	ASP	ASP	ASP	ASP	---	ASP	---	---	---	---	ALA	---	---	---	---	---	---
448	422	423	TRP	TRP	TRP	TRP	TRP	---	TRP	---	---	---	---	LEU	---	---	---	---	---	---
449	423	424	LYS	LYS	ASN	ASN	ASN	---	ASN	---	---	---	---	SER	---	---	---	---	---	---
450	424	425	---	---	---	---	---	---	---	---	---	---	---	SER	---	---	---	---	---	---
451	425	426	LYS	LYS	ASN	ASN	ASN	---	ASN	---	---	---	---	---	---	---	---	---	---	---
452	426	427	GLY	GLY	ARG	ARG	ARG	---	ARG	---	---	---	---	LEU	---	---	---	---	---	---
453	427	428	ASP	ASP	LYS	LYS	LYS	---	LYS	---	---	---	---	ASP	---	---	---	---	---	---
454	428	429	THR	THR	GLU	GLU														

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HEAVY CONSTANT CHAINS C83 REGION (cont'd)

EU INDEX	OU INDEX	123 RABBIT IGG	124 PGAMMA B1-12, 14'CL	125 RAB IGG	126 RAB IGG	127 P2A2 'CL	128 39-1A, 20B 'CL	129 PA19 'CL	130 CT-12	131 PIKA	132 HA-3	133 HA-11	134 HA-1	135 HA-5	136 HA-LT	137 SYRIAN IGM 'CL	138 GP IGG1	139 GP' IGG1	140 GP IGG1	141 MOC
361	341		GLY	GLY	GLY	GLY	GLY	---			GLY					---	GLY	GLY	GLY	---
362		340	---	---	---	---	---	VAL			---					SER	---	---	---	ASP
363	342	341	GLN	GLU	GLN	GLN	GLN	VAL			GLU					PRO	PRO	PRO	ALA	GLN
364	343	342	PRO	PRO	PRO	PRO	PRO	THR			ALA					SER	PRO	PRO	PRO	PRO
365	344	343	LEU	LEU	LEU	LEU	LEU	---			LEU					ARG	ARG	ARG	ARG	VAL
366	345	344	GLU	GLU	GLU	GLU	GLU	PRO			GLU					ASP	---	---	---	---
367	346	345	PRO	PRO	PRO	PRO	PRO	PRO			PRO					ILE	PRO	---	---	---
367A			---	---	---	---	---	---			---					---	---	---	---	---
367B			---	---	---	---	---	---			---					---	---	---	---	---
368	347	346	LYS	LYS	LYS	LYS	LYS	GLN			LYS					GLN	GLX	GLX	ASP	SER
369	348	347	VAL	VAL	VAL	VAL	VAL	VAL			VAL					ALA	VAL	VAL	VAL	ILE
370	349	348	TYR	TYR	TYR	TYR	TYR	HIS			TYR					PHE	TYR	TYR	TYR	PHE
371	350	349	THR	THR	THR	THR	THR	LEU			THR					PRO	LEU	LEU	THR	THR
372	351	350	MET	MET	MET	MET	MET	LEU			LEU					---	---	---	---	---
373	352	351	GLY	GLY	GLY	GLY	GLY	PRO			GLY					PRO	PRO	PRO	PRO	PRO
374	353	352	PRO	PRO	PRO	PRO	PRO	PRO			PRO					PRO	PRO	PRO	PRO	PRO
375	354	353	ARG	ARG	ARG	ARG	ARG	---			---					SER	---	---	---	---
376	355		GLU	GLU	GLU	GLU	GLU	SER			GLU					PHE	ASX	ASX	ASP	PHE
377	356	354	GLU	GLN	GLU	GLU	GLU	GLU			GLU					VAL	GLX	GLX	GLX	ALA
378	357	355	---	---	---	---	---	---			---					GLY	---	---	---	SER
379		356	---	---	---	---	---	---			---					---	---	---	---	---
380		357	LEU	LEU	LEU	LEU	LEU	ALA			LEU					PHE	LEU	LEU	LEU	---
381	358	358	SER	SER	SER	SER	SER	LEU			LEU					LEU	SER	SER	SER	ASN
382	359	359	SER	SER	SER	SER	SER	ASN			ASN					ASN	LYS	LYS	LYS	THR
383	360	360	---	---	---	---	---	---			---					---	---	---	---	---
384	361	361	ARG	ARG	ARG	ARG	ARG	GLU			GLU					LYS	LYS	LYS	SER	LYS
385	362	362	SER	SER	SER	SER	SER	GLN			GLN					SER	LYS	LYS	LYS	SER
386	363	363	VAL	VAL	VAL	VAL	VAL	VAL			VAL					ALA	VAL	VAL	VAL	ALA
387	364	364	SER	SER	SER	SER	SER	THR			THR					THR	SER	SER	SER	LYS
388	365	365	LEU	LEU	LEU	LEU	LEU	LEU			LEU					LEU	LEU	LEU	VAL	LEU
389	366	366	THR	THR	THR	THR	THR	THR			THR					THR	THR	THR	THR	SER
390	367	367	CYS	CYS	CYS	CYS	CYS	CYS			CYS					CYS	CYS	CYS	CYS	CYS
391	368	368	MET	MET	MET	MET	MET	LEU			LEU					LEU	MET	MET	LEU	LEU
392	369	369	ILE	ILE	ILE	ILE	ILE	VAL			VAL					VAL	ILE	ILE	ILE	VAL
393	370	370	ASN	ASP	ASN	ASN	ASN	ARG			ARG					THR	THR	THR	ILE	THR
394	371	371	GLY	GLY	GLY	GLY	GLY	GLY			GLY					ASN	GLY	GLY	ASN	ASP
395	372	372	PHE	PHE	PHE	PHE	PHE	PHE			PHE					LEU	PHE	PHE	PHE	LEU
396	373	373	TYR	TYR	TYR	TYR	TYR	SER			SER					ALA	TYR	TYR	TYR	ALA
397	374	374	PRO	PRO	PRO	PRO	PRO	PRO			PRO					THR	PRO	PRO	PRO	THR
398	375	375	SER	SER	SER	SER	SER	LYS			LYS					TYR	ALA	ALA	ALA	TYR
399	376	376	ASP	ASP	ASP	ASP	ASP	ASP			ASP					ASP	ASP	ASP	ASP	ASP
400	377		ILE	ILE	ILE	ILE	ILE	VAL			VAL					---	ILE	ILE	ILE	---
401	378	377	SER	SER	SER	SER	SER	LEU			LEU					THR	ASN	ASN	HIS	SER
402	379	378	VAL	VAL	VAL	VAL	VAL	VAL			VAL					LEU	VAL	VAL	VAL	VAL
403		379	---	---	---	---	---	---			---					ASN	---	---	---	THR
404		380	---	---	---	---	---	---			---					---	---	---	---	---
405	380	381	GLU	GLY	GLU	GLU	GLU	SER			GLU					ILE	SER	GLU	---	ILE
406	381	382	TRP	TRP	TRP	TRP	TRP	TRP			TRP					SER	TRP	TRP	TRP	TRP
407	382	383	GLU	GLU	GLU	GLU	GLU	ARG			GLU					SER	ASP	ASP	ALA	THR
408	383	384	LYS	LYS	LYS	LYS	LYS	HIS			LYS					SER	SER	SER	SER	ARG
409			---	---	---	---	---	---			---					---	---	---	---	---
410	384	385	ASN	ASP	ASN	ASN	ASN	GLN			GLN					ARG	SER	SER	ASN	GLU
411	385	386	GLY	GLY	GLY	GLY	GLY	GLY			GLY					SER	GLY	GLY	GLY	GLY
412			---	---	---	---	---	---			---					---	---	---	---	---
413			---	---	---	---	---	---			---					---	---	---	---	---
414	386	387	LYS	LYS	LYS	LYS	LYS	VAL			VAL					GLY	---	---	---	ASN
415	387	388	ALA	ALA	ALA	ALA	ALA	PRO			PRO					GLU	SER	SER	SER	GLY
416	388	389	GLU	GLU	GLU	GLU	GLU	GLU			GLU					PRO	ASP	ASP	GLU	ALA
417	389	390	ASP	ASP	ASP	ASP	ASP	ASP			ASP					LEU	---	---	---	LYS
418	390	391	ASN	ASN	ASN	ASN	ASN	SER			SER					GLU	---	---	---	LYS
419	391	392	TYR	TYR	TYR	TYR	TYR	PHE			PHE					THR	TYR	TYR	TYR	THR
420	392	393	LYS	LYS	LYS	LYS	LYS	LEU			LEU					LYS	LYS	LYS	LYS	HIS
421	393	394	THR	THR	THR	THR	THR	VAL			VAL					THR	ASN	ASN	ASN	THR
422	394	395	THR	THR	THR	THR	THR	TRP			TRP					LYS	THR	THR	THR	ASN
423	395	396	PRO	PRO	PRO	PRO	PRO	LYS			LYS					LEU	PRO	PRO	PRO	ILE
424	396	397	ALA	ALA	ALA	ALA	ALA	SER			SER					THR	PRO	PRO	PRO	SER
425	397	398	VAL	VAL	VAL	VAL	VAL	MET			MET					GLU	VAL	VAL	ILE	GLU
426	398	399	LEU	LEU	LEU	LEU	LEU	PRO			PRO					SER	PHE	PHE	GLU	SER
427	399	400	ASP	ASP	ASP	ASP	ASP	GLU			GLU					HIS	ASP	ASP	ASP	HIS
428	400	401	SER	SER	SER	SER	SER	SER			SER					PRO	SER	THR	ALA	PRO
429			---	---	---	---	---	---			---					---	---	---	---	---
430	401	402	ASP	ASP	ASP	ASP	ASP	GLN			GLN					ASN	ASP	ASP	ASP	ASN
431			---	---	---	---	---	---			---					---	---	---	---	---
432			---	---	---	---	---	---			---					---	---	---	---	---
433	402	403	GLY	GLY	GLY	GLY	GLY	ALA			ALA					GLY	GLU	GLY	GLY	GLY
434	403	404	SER	SER	SER	SER	SER	THR			THR					THR	THR	THR	THR	THR
435	404	405	TYR	TYR	TYR	TYR	TYR	TYR			TYR					PHE	PHE	PHE	PHE	PHE
436	405	406	PHE	PHE	PHE	PHE	PHE	ALA			ALA					SER	PHE	PHE	PHE	SER
437	406	407	LEU	LEU	LEU	LEU	LEU	ILE			ILE					ALA	LEU	LEU	LEU	ALA
438	407	408	TYR	TYR	TYR	TYR	TYR	THR			THR					ILE	TYR	TYR	TYR	MET
439	408	409	ASN	SER	SER	SER	SER	SER			SER					GLY	SER	SER	SER	GLY
440	409	410	LYS	LYS	LYS	LYS	LYS	LEU			LEU					GLU	ARG	ARG	LYS	GLU
441	410	411	LEU	LEU	LEU	LEU	LEU	LEU			LEU					ALA	LEU	LEU	LEU	ALA
442	411	412	SER	SER	SER	SER	SER	ARG			ARG					ASN	LYS	LYS	LYS	THR
443	412	413	VAL	VAL	VAL	VAL	VAL	VAL			VAL					VAL	VAL	VAL	VAL	VAL
444	413	414	PRO	PRO	PRO	PRO	PRO	PRO			PRO					CYS	ASP	ASP	ASP	CYS
445	414	415	THR	THR	THR	THR	THR	ALA			ALA					VAL	THR	THR	LYS	VAL
446	415	416	SER	SER	SER	SER	SER	GLU			GLU					GLU	ASN	ASN	SER	GLU
447	416	417	GLU	GLU	GLU	GLU	GLU	ASP			ASP					ASP	ALA	ALA	ALA	GLU
448	417	418	TRP	TRP	TRP	TRP	TRP	TRP			TRP					TRP	TRP	TRP	TRP	TRP
449	418	419	GLN	GLN	GLN	GLN	GLN	ASN			ASN					ASP	ASN	ASN	ASP	GLU
450		420	---	---	---	---	---	---			---					---	---	---	---	---
451	419	420	ARG	ARG	ARG	ARG	ARG	GLN			GLN					SER	ASP	ASN	GLN	SER
452	420	421	GLY	GLY	GLY	GLY	GLY	GLY			GLY					GLY	GLY	GLY	GLY	GLY
453	421	422	ASP	ASP	ASP	ASP	ASP	ASP			ASP					LYS	GLU	GLU	THR	GLU
454	422	423	VAL	VAL	VAL	VAL	VAL	THR			THR				</					

HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	142 PIG	143 SHEEP	144 HORSE	145 BOVINE	146 GOAT	147 CHICKEN	148 Elops	149 Re4b	150 Re20	151 Xenopus laevis	152 Xenopus laevis	153 Xenopus laevis	154 Xenopus laevis	155 Xenopus laevis	156 Xenopus laevis
IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG	IGG
361	341		GLY						ASF		THR	PRO				
362		340	---				VAL	---	VAL	---	ALA	ILE				
363	342	341	GLN				VAL	PRO	SER	---	ILE	THR				
364	343	342	ALA				GLN	GLU	CYS	---	THR	PRO				
365	344	343	ARG				GLN	ALA	ASP	---	PRO	THR				
366	345	344	GLU				ASP	GLN	LYS	---	VAL	SER				
367	346	345	PRO				ILE	ILE	LEU	---	VAL	ILE				
367A			---				---	---	---	---	---	---				
367B			---				---	---	---	---	---	---				
368	347	346	GLN				ALA	ASP	SER	---	---	GLN				
369	348	347	VAL				ILE	ALA	ILE	---	---	VAL				
370	349	348	TYR				ARG	LYS	THR	---	ASP	ILE				
371	350	349	VAL				ILE	ILE	---	---	VAL	THR				
372	351	350	LEU				ILE	SER	LEU	---	LEU	THR				
373	352	351	ALA				THR	PRO	PRO	---	PRO	PRO				
374	353	352	PRO				PRO	PRO	PRC	---	PRO	PRC				
375	354	353	PRO				SER	THR	GLN	---	SER	SER				
376	355		GLN				---	---	---	---	---	---				
377	356	354	GLU				PHE	PRO	VAL	---	PRO	LEU				
378	357	355	GLU				VAL	GLU	GLU	---	LYS	GLU				
379		356	---				ASP	GLU	GLN	---	ASP	SER				
380		357	---				ILE	LEU	LEU	---	LEU	ILE				
381	358	358	LEU				PHE	PHE	LEU	---	LEU	PHE				
382	359	359	SER				ILE	LEU	MET	---	VAL	GLU				
383	360	360	LYS				SER	GLN	GLU	---	THR	LYS				
384	361	361	SER				LYS	GLN	MET	---	LYS	LYS				
385	362	362	THR				SER	THR	THR	---	GLU	SER				
386	363	363	ALA				ALA	ARG	VAL	---	ALA	ALA				
387	364	364	SER				THR	THR	THR	---	LYS	THR				
388	365	365	VAL				LEU	LEU	LEU	---	VAL	LEU				
389	366	366	THR				THR	THR	THR	---	TYR	THR				
390	367	367	CYS				CYS	CYS	CYS	---	CYS	CYS				
391	368	368	LEU				ARG	LYS	LEU	---	VAL	LEU				
392	369	369	VAL				VAL	ILE	VAL	---	ILE	VAL				
393	370	370	THR				SER	THR	SER	---	SER	SER				
394	371	371	GLY				ASN	GLY	ASP	---	ARG	ASN				
395	372	372	PHE				MET	ALA	ALA	---	MET	MET				
396	373	373	TYR				VAL	VAL	PRO	---	ALA	ALA				
397	374	374	PRO				ASN	ASP	TYR	---	SER	ASN				
398	375	375	ASP				ALA	GLY	GLY	---	THR	SER				
399	376	376	TYR				ASP	VAL	ILE	---	ASP	GLU				
400	377		ILE				---	---	---	---	ASP	ASP				
401	378	377	ALA				GLY	ARG	---	---	LEU	LEU				
402	379	378	VAL				ASN	---	---	---	---	ARG				
403		379	---				GLU	VAL	THR	---	THR	---				
404		380	---				VAL	THR	VAL	---	VAL	ILE				
405	380	381	GLU				SER	TRP	SER	---	GLN	SER				
406	381	382	TRP				TRP	GLU	TRP	---	TRP	TRP				
407	382	383	GLN				TRP	VAL	LYS	---	SER	PHE				
408	383	384	LYS				LYS	GLY	ARG	---	ARG	LYS				
409			---				---	---	---	---	---	---				
410	384	385	ASN				GLU	SER	---	---	SER	LYS				
411	385	386	GLY				LYS	GLU	GLY	---	GLY	GLY				
412			GLN				---	---	---	---	---	---				
413			PRO				---	---	---	---	---	---				
414	386	387	GLU				GLY	VAL	ASN	---	LYS	THR				
415	387	388	SER				GLY	ARG	VAL	---	LYS	GLN				
416	388	389	GLU				VAL	PRO	VAL	---	ALA	GLU				
417	389	390	ASP				LEU	GLY	LEU	---	ALA	ILE				
418	390	391	LYS				GLU	GLN	VAL	---	ALA	PRO				
419	391	392	TYR				THR	PHE	SER	---	PHE	LEU				
420	392	393	GLY				ALA	ASP	TYR	---	ASP	LYS				
421	393	394	THR				LEU	GLU	ILE	---	SER	THR				
422	394	395	THR				GLY	GLN	GLN	---	ALA	GLU				
423	395	396	THR				LYS	LYS	PRO	---	PRO	LEU				
424	396	397	SER				ARG	MET	THR	---	GLU	GLY				
425	397	398	GLY				VAL	ILE	GLY	---	LYS	ASP				
426	398	399	LEU				LEU	SER	---	---	ALA	ALA				
427	399	400	ASP				GLN	LYS	---	---	TYR	ILE				
428	400	401	ALA				SER	LEU	---	---	---	TYR				
429			---				---	---	---	---	---	---				
430	401	402	ASP				ASN	LEU	---	---	---	ASN				
431			---				---	ILE	---	---	---	ASP				
432			---				---	ASP	---	---	ASP	ASN				
433	402	403	GLY				GLY	TYR	PRO	---	GLY	ARG				
434	403	404	SER				LEU	GLU	ALA	---	THR	THR				
435	404	405	TYR				TYR	GLU	ASP	---	PHE	TYR				
436	405	406	PHE				THR	TRP	ILE	---	THR	SER				
437	406	407	LEU				VAL	LYS	VAL	---	VAL	VAL				
438	407	408	TYR				ASP	ASN	GLN	---	LYS	LYS				
439	408	409	SER				GLY	ARG	SER	---	SER	GLY				
440	409	410	ARG				VAL	THR	LYS	---	THR	THR				
441	410	411	LEU				ALA	GLU	VAL	---	LEU	THR				
442	411	412	ARG				THR	TYR	ASN	---	LYS	THR				
443	412	413	VAL				VAL	THR	ILE	---	ILE	VAL				
444	413	414	ASP				CYS	CYS	SER	---	SER	CYS				
445	414	415	LYS				ALA	LYS	THR	---	PRO	ALA				
446	415	416	ASN				SER	VAL	GLN	---	GLY	ASP				
447	416	417	SER				GLU	GLU	ASP	---	ASP	GLU				
448	417	418	TRP				TRP	HIS	TRP	---	TRP	TRP				
449	418	419	GLN				ASP	SER	LEU	---	GLU	ASN				
			---				---	ASP	---	---	---	---				
			---				---	LEU	---	---	---	---				
450	419	420	GLU				GLY	PRO	SER	---	ASN	ASN				
451	420	421	GLY				ASP	SER	GLY	---	LYS	ASP				
452	421	422	ASP				GLY	PRO	ASP	---	GLN	LYS				
453	422	423	THR				GLY	LEU	TYR	---	---	---				
454	423	424	TYR				TYR	ARG	PHE	---	PHE	PHE				
455	424	425	ALA				VAL	THR	GLU	---	ASN	VAL				
456	425	426	CYS				CYS	SER	CYS	---	CYS	CYS				
457	426	427	VAL				LYS	TYR	ALA	---	LYS	LYS				
458	427	428	VAL				VAL	ARG	VAL	---	VAL	VAL				
459	428	429	MET				ASN	ARG	SER	---	VAL	GLU				
460	429	430	HIS	HIS	HIS		HIS	GLU	HIS	---	HIS	HIS				
461	430	431	GLU	GLU	GLU		PRO	CYS	ALA	---	PRO	THR				
462	431	432	ALA	ALA	ALA		ASP	GLY	ASP	---	ASP	GLU				
463	432	433	LEU	LEU	LEU		LEU	GLY	MET	---	LEU	LEU				
464	433	434	HIS	HIS	HIS		LEU	LYS	PRO	---	PRO	ALA				
465	434	435	ASN	ASN	ASN		PHE	TRP	LYS	---	SER	SER				
466	435	436	HIS	HIS	HIS		PRO	GLN	PRO	---	PRO	MET				
467	436	437	TYR	TYR	TYR		SER	THR	LYS	---	ILE	LYS				
468	437		THR	THR	THR		---	PRO	---	---	---	---				
469	438	438	GLN	GLN	GLN		GLU	THR	THR	---	---	GLU				
470	439	439	LYS	LYS	LYS		GLU	VAL	GLU	---	GLU	VAL				
471	440	440	SER	SER	SER		LYS	PHE	ARG	---	LYS	PHE				
472	441	441	ILE	VAL	THR		MET	ILE	ILE	---	SER	LEU				
473	442	442	SER	SER	SER		---	---	---	---	---	---				
474	443	443	LYS	LYS	LYS		ARG	LEU	ASN	---	GLN	PHE				
475	444	444	PRO	SER	SER		LYS	ALA	TRP	---	LYS	LYS				
476	445	445	PRO	PRO	ALA		THR	PRO	LYS	---	SER	GLU				

HEAVY CONSTANT CHAINS CH3 REGION (cont'd)

EU INDEX	OU INDEX	157 Xenopus laevis 'CL	158 Xenopus laevis 'CL	159 Xenopus laevis 'CL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
361	341				74	5	54 (GLY)	6.9
362					37	8	11 (SER)	2.7
363	342	340			89	14	33 (GLN), 32 (GLN)	38.39.
364	343	342			90	10, 11	43 (PRO)	21.23.
365	344	343			91	10	45 (ARG)	20.
366	345	344			92	13	24 (GLU), 23 (GLU)	50.52.
367	346	345			92	9	50 (PRO)	1.7.
367A					5	4	2 (THR)	
367B					5	1	5 (PRO)	
368	347	346			91	10	43 (GLN), 40 (GLN)	21.23.
369	348	347			93	6	65 (VAL)	8.6
370	349	348			94	10	57 (TYR)	16.
371	350	349			94	7	39 (THR)	17.
372	351	350			94	5	48 (LEU)	9.8
373	352	351			93	7	68 (PRO)	9.6
374	353	352			93	3	87 (PRO)	3.2
375	354	353			93	4	51 (SER)	1.3
376	355	354			57	6	24 (ARG)	14.
377	356	355			88	11, 13	32 (GLU), 28 (GLU)	30.41.
378	357	356			91	10	49 (GLU), 45 (GLU)	19.20.
379		356			36	5	14 (GLU)	13.
380		357			48	3	28 (LEU)	8.6
381	358	358			92	10	26 (MET)	25.
382	359	359			92	10	27 (LEU)	34.
383	360	360			92	10, 11	32 (LYS)	29.32.
384	361	361			91	10	33 (LYS)	28.
385	362	362			91	8	32 (SER)	23.
386	363	363			91	8	48 (VAL)	15.
387	364	364			84	4	41 (SER)	10.
388	365	365			92	4	81 (LEU)	4.5
389	366	366			92	6	83 (THR)	6.7
390	367	367			92	6	92 (CYS)	1.
391	368	368			91	6	65 (LEU)	8.4
392	369	369			91	5	66 (VAL)	6.9
393	370	370			92	9	22 (THR)	38.
394	371	371			92	6	52 (GLY)	11.
395	372	372			92	1	61 (PHE)	7.5
396	373	373			92	1	21 (TYR)	33.
397	374	374			92	6	67 (PRO)	8.2
398	375	375			93	10	30 (SER)	31.
399	376	376			93	10	59 (ASP), 56 (ASP)	16.17.
400	377	377			66	4	45 (ILE)	5.9
401	378	378			91	10	21 (ALA)	43.
402	379	379			90	9	68 (VAL)	12.
403		379			31	5, 6	14 (ASN), 13 (+)	11.14.
404		380			31	4	14 (ILE)	8.9
405	380	381.			92	10	38 (GLU)	26.
406	381	382			91	2	86 (TRP)	2.1
407	382	383			90	13	24 (GLU), 23 (GLU)	49.51.
408	383	384			81	10	34 (SER)	24.
409					16	6	8 (GLN)	12.
410	384	385			10	10	27 (ASN), 26 (ASN)	32.33.
411	385	386			87	8, 9	34 (GLY)	20.23.
412					19	4	10 (GLN)	7.6
413					28	6	12 (GLU)	14.
414	386	387			86	11	21 (GLY)	45.
415	387	388			88	12	28 (PRO)	38.
416	388	389			88	11, 12	35 (GLU), 34 (GLU)	28.31.
417	389	390			83	5	18 (GLU)	41.
418	390	391			86	10	37 (ASN), 36 (ASN)	23.24.
419	391	392			87	10	47 (TYR)	19.
420	392	393			89	11	40 (LYS)	24.
421	393	394			88	12	44 (THR)	24.
422	394	395			88	10, 11	37 (THR)	24.26.
423	395	396			88	10	32 (PRO)	27.
424	396	397			88	11	37 (PRO)	26.
425	397	398			88	12	24 (VAL)	44.
426	398	399			87	13	33 (LEU)	34.
427	399	400			88	12	37 (ASP)	29.
428	400	401			84	11	35 (SER)	26.
429		401			16	3	11 (SER)	4.4
430	401	402			85	6	42 (ASP), 40 (ASP)	12.13.
431					14	2	11 (GLY)	3.8
432					15	2	8 (THR)	9.4
433	402	403			88	9	54 (GLY)	15.
434	403	404			88	7	45 (THR)	12.
435	404	405			88	7	45 (PHE)	14.
436	405	406			88	8	41 (PHE)	17.
437	406	407			88	7	30 (LEU)	21.
438	407	408			89	10	42 (TYR)	21.
439	408	409			88	4	72 (SER)	4.9
440	409	410			89	5	38 (LYS)	16.
441	410	411			88	5	72 (LEU)	6.1
442	411	412			87	8	23 (ARG)	30.
443	412	413			89	5	76 (VAL)	5.9
444	413	414			90	10	26 (ASP)	35.
445	414	415			90	7	31 (LYS)	25.
446	415	416			90	11	33 (SER)	30.
447	416	417			91	10	36 (ASP), 31 (ASP)	25.29.
448	417	418			89	4	82 (TRP)	4.3
449	418	419			91	12	25 (GLN), 24 (GLN)	44.45.
450	419	420			1	1	1 (ASP)	
451	420	421			1	1	1 (LEU)	
452	421	422			91	10	28 (GLN), 27 (GLN)	32.34.
453	422	423			90	8	71 (GLY)	10.
454	423	424			89	9	25 (ASP), 24 (+)	33.34.
455	424	425			91	11	25 (THR)	39.
456	425	426			90	7	60 (PHE)	4.5
457	426	427			90	2	36 (SER)	17.
458	427	428			89	10	89 (CYS)	2.
459	428	429			91	10	35 (SER)	2.
460	429	430			92	10	90 (VAL)	2.
461	430	431			93	3	26 (MET)	35.
462	431	432			94	8	91 (HIS)	3.1
463	432	433			94	8	59 (GLU)	13.
464	433	434			95	5	42 (ALA)	13.
465	434	435			95	7	81 (LEU)	5.9
466	435	436			95	10	43 (PRO)	15.
467	436	437			95	12	45 (ASN)	21.
468	437	438			94	10	38 (HIS)	30.
469	438	439			94	6	26 (TYR)	36.
470	439	440			93	7	50 (THR)	7.6
471	440	441			90	6	43 (GLN)	15.
472	441	442			95	7	64 (LYS)	8.4
473	442	443			94	9	53 (SER)	13.
474	443	444			95	8	52 (ILE)	16.
475	444	445			95	7	1 (ILE)	
476	445	446			95	8	64 (SER)	12.
477	446	447			95	8	39 (ARG)	17.
478					95	10	42 (SER)	18.
					66	3	44 (PRO)	22.
					43	4	59 (GLY)	3.4
							36 (LYS)	4.8

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